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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: Murphy et al.

Application No.: To be assigned

Group Art Unit: To be assigned

Filed: April 27, 1999

Examiner: To be assigned

For: Nr-CAM GENE, NUCLEIC ACIDS AND NUCLEIC ACID PRODUCTS FOR THERAPEUTIC AND DIAGNOSTIC USES FOR TUMORS

Attorney Docket No.: 8511-021

TRANSMITTAL OF SEQUENCE LISTING UNDER 37 C.F.R. § 1.821

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

In accordance with 37 C.F.R. § 1.821, Applicant, in connection with the above-identified patent application, submits herewith a Sequence Listing in paper and computer readable form pursuant to 37 C.F.R. §§ 1.821(c) and (e).

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 C.F.R. §§ 1.821(c) and (e), respectively, are the same.

Respectfully submitted,

Date: April 27, 1999

31,232
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Enclosure

SEQUENCE LISTING

<110> Murphy, Gerald P.
Boynton, Alton L.
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<120> Nr-CAM GENE, NUCLEIC ACIDS AND NUCLEIC ACID PRODUCTS
FOR THERAPEUTIC AND DIAGNOSTIC USES FOR TUMORS

<130> 8511-021

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acc aaa gaa aaa ctt gaa cca atc aca ctt caa agt ggt cag tct tta   603
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gta ctt ccc tgc aga ccc cca att gga tta cca cca cct ata ata ttt   651
Val Leu Pro Cys Arg Pro Pro Ile Gly Leu Pro Pro Pro Ile Ile Phe
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caa ggt ttg aat ggg gac ctt tat ttt tcc aat gtc ctc cca gag gac   747
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Ile Gln Gln Lys Gln Pro Ile Ser Val Lys Val Ile Ser Val Asp Glu
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aga gtt aaa gcg gct cca tac tgg atc aca gcc cct caa aat ctt gtg   1227
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            370                 375                 380

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gcc cct gat gac ccc agc aga aaa ata gat ggc gat acc att att ttt   1371
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aat gaa tat gga tat tta ctg gca aac gca ttt gta aat gtg ctg gct   1467
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cca acc atc gag tgg ttt aaa gga gct aaa gga agt gct ctt cat gaa   1611
Pro Thr Ile Glu Trp Phe Lys Gly Ala Lys Gly Ser Ala Leu His Glu
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gat att tat gtt tta cat gaa aat gga act ttg gaa atc aaa gat gct   1659
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tcc ttt gaa tgc aaa gtg aaa cat gat cac acc tta tcc ctc act gtc   1851
Ser Phe Glu Cys Lys Val Lys His Asp His Thr Leu Ser Leu Thr Val
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Val Asp Lys Asp His Leu Val Val Ala Asp Val Ser Asp Asp Asp Ser
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agc gct gtg ctt agc gtt gtt gct cct act cca act cca gct ccc gtt   2043
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ccc att aca aaa ttc atc atc gaa tat gaa gat gca atg cac aag cca   2187
Pro Ile Thr Lys Phe Ile Ile Glu Tyr Glu Asp Ala Met His Lys Pro
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Gly Leu Trp His His Gln Thr Glu Val Ser Gly Thr Gln Thr Thr Ala
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cag ctg aag ctg tct cct tac gtg aac tac tcc ttc cgc gtg atg gca   2283
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gtg aac agc att ggg aag agc ttg ccc agc gag gcg tct gag cag tat   2331
Val Asn Ser Ile Gly Lys Ser Leu Pro Ser Glu Ala Ser Glu Gln Tyr
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ttg acg aaa gcc tca gaa cca gat aaa aac ccc aca gct gtg gaa gga   2379
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Ser Lys Tyr Ile Val Ser Gly Thr Pro Thr Phe Val Pro Tyr Leu Ile
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gtc atg gga cat tct gga gaa gac ctc cca atg gtg gct cct ggg aac   2667
Val Met Gly His Ser Gly Glu Asp Leu Pro Met Val Ala Pro Gly Asn
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gtg cgt gtg aat gtg gtg aac agt acc tta gcc gag gtg cac tgg gac   2715
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Pro Val Pro Leu Lys Ser Ile Arg Gly His Leu Gln Gly Tyr Arg Ile
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tac tat tgg aag acc cag agt tca tct aaa aga aac aga cgt cac att   2811
Tyr Tyr Trp Lys Thr Gln Ser Ser Ser Lys Arg Asn Arg Arg His Ile
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gag aaa aag atc ctc acc ttc caa ggc agc aag act cat ggc atg ttg   2859
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ccg ggg cta gag ccc ttt agc cac tac aca ctg aat gtc cga gtg gtc   2907
Pro Gly Leu Glu Pro Phe Ser His Tyr Thr Leu Asn Val Arg Val Val
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cca gaa gga gtc ccc agt gct ccc tcg tct ttg aag att gtg aat cca   3003
Pro Glu Gly Val Pro Ser Ala Pro Ser Ser Leu Lys Ile Val Asn Pro
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aca ctg gac tct ctc act ttg gaa tgg gat cca ccg agc cac ccg aat   3051
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His Glu Leu Gly Pro Leu Val Asp Leu Lys Ile Pro Ala Asn Lys Thr
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cgg tgg act tta aaa aat tta aat ttc agc act cga tat aag ttt tat   3195
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ttc tat gca caa aca tca gca gga tca gga agt caa att aca gag gaa   3243
Phe Tyr Ala Gln Thr Ser Ala Gly Ser Gly Ser Gln Ile Thr Glu Glu
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Ala Gly Lys Val Gln Ala Val Asn Thr Arg Ile Ser Asn Leu Thr Ala
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Lys Gly Leu Met Pro Gly Thr Ala Tyr Lys Val Arg Val Gly Ala Val
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Gly Thr Phe Gly Glu Tyr Ser Asp Ala Glu Asp His Lys Pro Leu Lys
1215                1220                1225                1230

aaa gga agt cga act cct tca gac agg act gtg aaa aaa gaa gat agt   3867
Lys Gly Ser Arg Thr Pro Ser Asp Arg Thr Val Lys Lys Glu Asp Ser
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           1250                1255                1260

gag gat ggc tcc ttt att gga caa tac agt ggt aag aaa gag aaa gag   3963
Glu Asp Gly Ser Phe Ile Gly Gln Tyr Ser Gly Lys Lys Glu Lys Glu
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Met Asn Ser Phe Val
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Leu Leu Glu Asp Leu Val Gln Pro Pro Thr Ile Thr Gln Gln Ser Pro
         35                  40                  45

Lys Asp Tyr Ile Ile Asp Pro Arg Glu Asn Ile Val Ile Gln Cys Glu
     50                  55                  60

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His Phe Asp Ile Asp Lys Asp Pro Leu Val Thr Met Lys Pro Gly Thr
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Glu Gly Val Tyr Gln Cys Thr Ala Arg Asn Glu Arg Gly Ala Ala Val
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Ser Asn Asn Ile Val Val Arg Pro Ser Arg Ser Pro Leu Trp Thr Lys
    130                 135                 140

Glu Lys Leu Glu Pro Ile Thr Leu Gln Ser Gly Gln Ser Leu Val Leu
145                 150                 155                 160

Pro Cys Arg Pro Pro Ile Gly Leu Pro Pro Pro Ile Ile Phe Trp Met
                165                 170                 175

Asp Asn Ser Phe Gln Arg Leu Pro Gln Ser Glu Arg Val Ser Gln Gly
            180                 185                 190

Leu Asn Gly Asp Leu Tyr Phe Ser Asn Val Leu Pro Glu Asp Thr Arg
        195                 200                 205

Glu Asp Tyr Ile Cys Tyr Ala Arg Phe Asn His Thr Gln Thr Ile Gln
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Gln Lys Gln Pro Ile Ser Val Lys Val Ile Ser Val Asp Glu Leu Asn
225                 230                 235                 240

Asp Thr Ile Ala Ala Asn Leu Ser Asp Thr Glu Phe Tyr Gly Ala Lys
                245                 250                 255

Ser Ser Arg Glu Arg Pro Pro Thr Phe Leu Thr Pro Glu Gly Asn Ala
            260                 265                 270

Ser Asn Lys Glu Glu Leu Arg Gly Asn Val Leu Ser Leu Glu Cys Ile
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Ala Glu Gly Leu Pro Thr Pro Ile Ile Tyr Trp Ala Lys Glu Asp Gly
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Met Leu Pro Lys Asn Arg Thr Val Tyr Lys Asn Phe Glu Lys Thr Leu
305                 310                 315                 320

Gln Ile Ile His Val Ser Glu Ala Asp Ser Gly Asn Tyr Gln Cys Ile
                325                 330                 335

Ala Lys Asn Ala Leu Gly Ala Ile His His Thr Ile Ser Val Arg Val
            340                 345                 350

Lys Ala Ala Pro Tyr Trp Ile Thr Ala Pro Gln Asn Leu Val Leu Ser
        355                 360                 365

Pro Gly Glu Asp Gly Thr Leu Ile Cys Arg Ala Asn Gly Asn Pro Lys
    370                 375                 380

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Val Gln Glu Arg Ser Ser Ala Val Tyr Gln Cys Asn Ala Ser Asn Glu
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Pro Arg Ile Leu Thr Pro Ala Asn Thr Leu Tyr Gln Val Ile Ala Asn
    450                 455                 460

Arg Pro Ala Leu Leu Asp Cys Ala Phe Phe Gly Ser Pro Leu Pro Thr
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Ile Glu Trp Phe Lys Gly Ala Lys Gly Ser Ala Leu His Glu Asp Ile
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Tyr Val Leu His Glu Asn Gly Thr Leu Glu Ile Lys Asp Ala Thr Trp
            500                 505                 510

Ile Val Lys Glu Ile Pro Val Ala Gln Lys Asp Ser Thr Gly Thr Tyr
        515                 520                 525

Thr Cys Val Ala Arg Asn Lys Leu Gly Met Ala Lys Asn Glu Val His
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Leu Gln Pro Glu Tyr Ala Val Val Gln Arg Gly Ser Met Val Ser Phe
545                 550                 555                 560

Glu Cys Lys Val Lys His Asp His Thr Leu Ser Leu Thr Val Leu Trp
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Leu Lys Asp Asn Arg Glu Leu Pro Ser Asp Glu Arg Phe Thr Val Asp
            580                 585                 590

Lys Asp His Leu Val Val Ala Asp Val Ser Asp Asp Asp Ser Gly Thr
        595                 600                 605

Tyr Thr Cys Val Ala Asn Thr Thr Leu Asp Ser Val Ser Ala Ser Ala
    610                 615                 620

Val Leu Ser Val Val Ala Pro Thr Pro Thr Pro Ala Pro Val Tyr Asp
625                 630                 635                 640

Val Pro Asn Pro Pro Phe Asp Leu Glu Leu Thr Asp Gln Leu Asp Lys
                645                 650                 655

Ser Val Gln Leu Ser Trp Thr Pro Gly Asp Asp Asn Asn Ser Pro Ile
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    770                 775                 780

Asp Gly Asp Asp Glu Trp Thr Ser Val Val Val Ala Asn Val Ser Lys
785                 790                 795                 800

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Pro Leu Lys Ser Ile Arg Gly His Leu Gln Gly Tyr Arg Ile Tyr Tyr
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Gly Val Pro Ser Ala Pro Ser Ser Leu Lys Ile Val Asn Pro Thr Leu
945                 950                 955                 960

Asp Ser Leu Thr Leu Glu Trp Asp Pro Pro Ser His Pro Asn Gly Ile
                965                 970                 975

Leu Thr Glu Tyr Thr Leu Lys Tyr Gln Pro Ile Asn Ser Thr His Glu
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Leu Gly Pro Leu Val Asp Leu Lys Ile Pro Ala Asn Lys Thr Arg Trp
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Ala Gln Thr Ser Ala Gly Ser Gly Ser Gln Ile Thr Glu Glu Ala Val
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Thr Thr Val Asp Glu Ala Gly Ile Leu Pro Pro Asp Val Gly Ala Gly
1045 1050 1055

Lys Val Gln Ala Val Asn Thr Arg Ile Ser Asn Leu Thr Ala Ala Ala
1060 1065 1070

Ala Glu Thr Tyr Ala Asn Ile Ser Trp Glu Tyr Glu Gly Pro Glu His
1075 1080 1085

Val Asn Phe Tyr Val Glu Tyr Gly Val Ala Gly Ser Lys Glu Glu Trp
1090 1095 1100

Arg Lys Glu Ile Val Asn Gly Ser Arg Ser Phe Phe Gly Leu Lys Gly
105 1110 1115 1120

Leu Met Pro Gly Thr Ala Tyr Lys Val Arg Val Gly Ala Val Gly Asp
1125 1130 1135

Ser Gly Phe Val Ser Ser Glu Asp Val Phe Glu Thr Gly Pro Ala Met
1140 1145 1150

Ala Ser Arg Gln Val Asp Ile Ala Thr Gln Gly Trp Phe Ile Gly Leu
1155 1160 1165

Met Cys Ala Val Ala Leu Leu Ile Leu Ile Leu Leu Ile Val Cys Phe
1170 1175 1180

Ile Arg Arg Asn Lys Gly Gly Lys Tyr Pro Val Lys Glu Lys Glu Asp
185 1190 1195 1200

Ala His Ala Asp Pro Glu Ile Gln Pro Met Lys Glu Asp Asp Gly Thr
1205 1210 1215

Phe Gly Glu Tyr Ser Asp Ala Glu Asp His Lys Pro Leu Lys Lys Gly
1220 1225 1230

Ser Arg Thr Pro Ser Asp Arg Thr Val Lys Lys Glu Asp Ser Asp Asp
1235 1240 1245

Ser Leu Val Asp Tyr Gly Glu Gly Val Asn Gly Gln Phe Asn Glu Asp
1250 1255 1260

Gly Ser Phe Ile Gly Gln Tyr Ser Gly Lys Lys Glu Lys Glu Pro Ala
265 1270 1275 1280

Glu Gly Asn Glu Ser Ser Glu Ala Pro Ser Pro Val Asn Ala Met Asn
1285 1290 1295

Ser Phe Val

<210> 3

<211> 38
<212> DNA
<213> Homo sapiens

<400> 3
tctcatacta tgaacatatg ggtagagagt atattttc 38

<210> 4
<211> 123
<212> DNA
<213> Rattus norvegicus

<400> 4
tctcatacta tggacatatg ggtagaaaga atgttttctg cggtatatga gtattataag 60

aacagagcaa gaacataact cagtcagtca gatgatacgt taatatgaac tggggtgaaa 120

agg 123

<210> 5
<211> 176
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: clone D4-1

<400> 5
tctcatacta tgaacatatg ggtagagagt atattttctg ctgtatgtta gtattatgag 60

aatagttaca gcaaaaacat aactcagtca aagtatatgt taatatgaac tggaatgcaa 120

aagtgcatac tttttcattc aaaatgggta ttcttgattt cctaaaaaaa aaaaaa 176

<210> 6
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 6
tagatacaac tagtcaatgc ctctaatgaa tatggata 38

<210> 7
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 7

agatagatcc gcggaatagt aaatccgata gccttgta 38

<210> 8
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
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<222> (1)
<223> n=a, c, g, or t

<400> 8
ngctgctctc atact 15

<210> 9
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 9
aacatatggg tagagagtat attt 24

<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 10
ctttgcattc cagttcatat taa 23

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 11
tgtggtgaca gatcacggct 20

<210> 12
<211> 21

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 12
cagctcaaac ctgtgatttc c 21

<210> 13
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 13
aataggtatt ggtgaattta aagactcact ctccataaat gctacgaata ttaaacactt 60

<210> 14
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 14
cggagcaata tgaaatgatc t 21

<210> 15
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 15
gcaaatacag ctcctattg 19

<210> 16
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 16
gctgtatgtt agtattatga gaatagttac agcaaaaaca taa 43

<210> 17
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 17
taggcctgac tggcattgta ttagcaaact catcactaga 40

<210> 18
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 18
tagatacaac tagtctaatg cagcttaaaa taatgcc 37

<210> 19
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 19
agatagatcc gcggatatcc atattcatta gaggcattg 39

<210> 20
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 20
tagatacaac tagtcaatgc ctctaatgaa tatggata 38

<210> 21
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 21
agatagatcc gcggaatagt aaatccgata gccttgta 38

<210> 22
<211> 61
<212> DNA
<213> Homo sapiens

<220>
<223> Description of Artificial Sequence: primer

<400> 22
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c 61

<210> 23
<211> 19
<212> DNA
<213> Homo sapiens

<400> 23
cattagcatc ttaactcct 19

<210> 24
<211> 21
<212> DNA
<213> Homo sapiens

<400> 24
tcggcattat tttaagctgc a 21

<210> 25
<211> 17
<212> DNA
<213> Homo sapiens

<400> 25
gcagataagc gcttctt 17

<210> 26
<211> 20
<212> DNA
<213> Homo sapiens

<400> 26
actagagata cagatcatat 20

<210> 27
<211> 20
<212> DNA
<213> Homo sapiens

<400> 27
catatacgat cgatcgatgc 20

<210> 28
<211> 20
<212> DNA
<213> Homo sapiens

<400> 28
gatagtgctg atcgatgcta 20

<210> 29
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 29
catacgaatt ctagatacaa ctagtctaat gcagcttaaa ataatgcc 48

<210> 30
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 30
agatagatcc gcggatatcc atattcatta gaggcattgg gatcccatac 50

<210> 31
<211> 1371
<212> DNA
<213> Homo sapiens

<400> 31
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atgattagtg cactggaagt acctcttgat ccaaaacttc ttgaagactt ggtacagcct 120

ccaaccatca cccaacagtc tccaaaagat tacattattg accctcggga gaatattgta 180

atccagtgtg aagccaaagg gaaaccgccc ccaagctttt cctggacccg taatgggact 240

cattttgaca tcgataaaga ccctctggtc accatgaagc ctggcacagg aacgctcata 300

attaacatca tgagcgaagg gaaagctgag acctatgaag gagtctatca gtgtacagca 360

aggaacgaac gcggagctgc agtttctaat aacattgttg tccgcccatc cagatcacca 420

ttgtggacca aagaaaaact tgaaccaatc acacttcaaa gtggtcagtc tttagtactt 480

ccctgcagac ccccaattgg attaccacca cctataatat tttggatgga taattccttt 540

caaagacttc cacaaagtga gagagtttct caaggtttga atggggacct ttatttttcc 600

aatgtcctcc cagaggacac ccgcgaagac tatatctgtt atgctagatt taatcatact 660

caaaccatac agcagaagca acctatttct gtgaaggtga tttcagtgga tgaattgaat 720

gacactatag ctgctaattt gagtgacact gagttttatg gtgctaaatc aagtagagag 780

aggccaccaa cattttaac tccagaaggc aatgcaagta acaaagagga attaagagga 840

aatgtgcttt cactggagtg cattgcagaa ggactgccta ccccaattat ttactgggca 900

aaggaagatg gaatgctacc caaaaacagg acagtttata agaactttga gaaaaccttg 960

cagatcattc atgtttcaga agcagactct ggaaattacc aatgtatagc aaaaaatgca 1020

ttaggagcca tccaccatac catttctgtt agagttaaag cggctccata ctggatcaca 1080

gcccctcaaa atcttgtgct gtccccagga gaggatggga ccttgatctg cagagctaat 1140

ggcaacccca aacccagaat tagctggtta acaaatggag tcccaataga aattgcccct 1200

gatgacccca gcagaaaaat agatggcgat accattattt tttcaaatgt tcaagaaaga 1260

tcaagtgcag tatatcagtg caatgcctct aatgaatatg gatatttact ggcaaacgca 1320

tttgtaaatg tgctggctga gccaccacga atcctcacac ctgcaaacac a 1371

<210> 32
<211> 1371
<212> DNA
<213> Rattus norvegicus

<400> 32
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atgatcagcg ctctggatgt tcctcttgat ccaaagctcc ttgatgactt ggtacagcct 120

ccaactatca ctcaacagtc accaaaagac tacatcattg acccacggga gaatattgta 180

atccaatgtg aggccaaagg gaaacctcct ccaagctttt cctggactcg taacggaaca 240

cattttgaca tagacaaaga ccctctggtc actatgaagc ctggctcagg aacccttgtc 300

atcaacatca tgagtgaagg aaaggcggag acctatgaag gggtttacca gtgcactgca 360

aggaatgagc gcggagctgc tgtctccaat aacattgttg tccgcccctc taggtcaccc 420

ttgtggacca aggaaagact tgaaccaata atcctccgaa gtggtcagtc actagtacta 480

ccatgtaggc ctccaattgg attaccaccg gccataatat tttggatgga taactccttt 540

caaagactgc cacagagtga gcgggtttcc caaggactga atggagacct ttacttctcc 600

aatgtcctcc cagaggacac ccgtgaggac tacatctgct atgccagatt taatcacact 660

caaacaattc aacagaaaca acctatttct ctgaaggtga tttcagtgga tgaattgaat 720

gacactatag ctgctaattt gagtgacact gagttttatg gtgctaaatc tagtaaagag 780

aggccaccaa catttctaac tccagagggc aatgaaagtc acaaggaaga attaagagga 840

aacgtgcttt ccctggagtg cattgcagaa ggcctaccta ctccagttat ttactggatc 900

aaggaagatg gaacgcttcc tgtcaaccgg acgttttatc ggaactttaa gaaaaccttg 960

cagatcattc atgtctctga agcagactct ggaaattatc agtgcatagc aaaaaacgca 1020

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gcacctcaca acctcgtgct ttccccaggg gagaatggga ccctcatctg cagagctaac 1140

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gatgacccca gccgaaaaat cgatggtgat accattatgt tttcaaatgt tcaagaaagc 1260

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